

Figure 1A

1	CCACTGTGCTGGAAATTGGCACGGACAGGCGAACGGACGTTAAAGTGAGAAAAGAAACCGG	60
61	TAAATCAGAGATCCCAAGCAAGCGCGTGCATGATAGCGAAGAAAAAGCTATCCG	120
121	TTTCAGTTAACTACTTACCAAGATTGAATTGCCATCGGGCAAATTACTAAAAATACAT	180
181	AAGTGCAACTCGTCCACTGTGTGTTGTGTTTTTTTTGGTTTCGCTGTGCC	240
241	TTTATCGCAAACAAGAACTGATAAAACTAGAAAATATCTTGAGAAACTTGTTCGCGCT	300
301	TTTCTTTGCTAATTGCCATCGCGGAAGAGAGAAAACAAGCAGTAGACAAAACAAGTGTG	360
361	GTAATACAATCTGAAAAGGGCACCATCAGCAGCCCCAGGGGTTATCTATATAGATGTCG	420
421	CAGCTTATCATCTCATGCTGTGAGGTTGTTCTGTGTGCTCGTGTAGTATCTTAAAT	480
481	ACATAGAGTGTGTTCATATAAAGTGCACAAAGCTCGATTGAAACAGCTGTCGAGTGCC	540
541	CTTGAGTGGTGGCAAGATCGTCATCATCATCATCGTCGTCAATTACAACAGAACAGC	600
601	ATCAGCATCTGGAGGCCCGGATGCTCTAAGATCCCCAGTGTTCATCAATTATGACTGCC	660
1	<u>M T A</u>	3
661	GAGACCCTCAAGCCGTTATAACGCCAACGAGTGCCAACGATGGTTTCCGGCCAAA	720
4	E T L K P F I T P T S A N D D D G F P A K	23
721	GCGACCAGCACGGCGACCGCCCAGCGACCGACCCGCCAGCTGATCCCCCTGGTTTGGGG	780
24	<u>A T S T A T A Q R R T R Q L I P L V L G</u>	43
781	TTCATCGGTCTGGGCTGGTCGTTGCCATTCTCGCACTAACGATCTGGCAGACAACGCGT	840
44	<u>F I G L G L V V A I L A L T I W Q T T R</u>	63
841	GTATCGCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAG	900
64	V S H L D K E L K S L K R V V D N L Q Q	83
901	CGTTGGGATAAACTATCTGGACGAGTTGACGAGTCCAAAAGGAGTACGAGAACGCC	960
84	R L G I N Y L D E F D E F Q K E Y E N A	103
961	CTCATCGACTATCCAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGACGACGATGGC	1020
104	L I D Y P K K V D G L T D E E D D D D G	123

Figure 1B

1021	GATGGTCTGGATTCCATTGCGGACGACGAGGACGACGACGTAGCTATA	GCTCTGTGGAT	1080
124	D G L D S I A D D E D D D V S Y S S V D		143
1081	GATGTTGGCGCAGACTACGAGGACTACACCGATATGTTAAATAAACTCAACA	ATGCACAT	1140
144	D V G A D Y E D Y T D M L N K L N N A H		163
1141	ACCGGCACCACGCCAACATCTGAGACCACTGCTGAGGGCGAGGGCGAGACGGACAGTGCA		1200
164	T G T T P T S E T T A E G E G E T D S A		183
1201	TCCTCAGCCTCAAATGATGACAATGTGTCGATGACTTACCA	GCTCAGATGCCCTCAAA	1260
184	S S A S N D D N V F D D F T S S D A L K		203
1261	AAGAAGCAGGAGAGAAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATT		1320
204	K K Q E R K S R S I A D V R N E E Q N I		223
1321	CAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAGCTTCAAAGAGAGC		1380
224	Q G N H T E L Q E K S S N E A A S K E S		243
1381	CCTGCAGCACTTCACCTCCGTCGAGAATGCATTCCGCCATGCCACCTCGTAGTCCGC		1440
244	P A A L H L R R R M H S R H R H L V V R		263
1441	AAAGCCAGATCCGAGGA	CTCGAGGCCAGCAGCCCATTCCACTTGAGCAGCAGGCCGT	1500
264	K A R S E D S R P A A H F H L S S R R R		283
1501	CACCAAGAAAGTATGGGCTACCATGGAGATATGTACATAGAAAATGATAGGGAGAGATGC		1560
284	H Q E S M G Y H G D M Y I E N D R E R C		303
1561	TCTTATCAGGGACACTTCAAACGCGCGATGGCGTATTGACGGTGACCAATGCAGGC	TA	1620
304	S Y Q G H F Q T R D G V		323
1621	TATTACGTATACGCCAGATATGGGGCTACAACTCGCACGACCAGAACGGATTATCGTC		1680
324	 G Y N S H D Q N G F I V		343
1681	TTTCAAGGAGACACTCCATTCTGCAGTGCTTGAACACGGTCCCCACCAACATGCCACAT		1740
344	F Q G D T P F L Q C L N T V P T N M P H		363
1741	AAGGTGCACACCTGCCACACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGGATCCAT		1800
364	K V H T C H T S G L I H L E R N E R I H		383
1801	CTGAAGGACATTACAACGATCGCAATGCAGTTCTGCGGGAGGGAAACAACCGAAGCTAC		1860
384	L K D I H N D R N A V L R E G N N R S Y		403

Figure 1C

1861	TTTGGCATCTCAAGGTGTAAATTGGAGAGATTATCCCCGGTCAGAAGATGGAATACCAG	1920
404	F G I F K V	409
1921	TTTAAGCTTTGTCCCCGCGACTGCTCGTGAATGCGATTCATGCCAGCGTGAATCCATT	1980
1981	AGTCGTAGTACCTAGTCAGTCACCTCAAACCTAACCTCAATCGGAATCGTGCATACT	2040
2041	GCATTAGTCAGAAGACGGAGGAAAATCATATTATTTGTATATACTCGTTCGACTCTAA	2100
2101	AAAGTGAATAAAATATATGTAGCTATTAAAAAAAAAAAAAAAAAAAAAAC	2160
2161	CTCGAG 2166	

Figure 2A

1	ATGACTGCCGAGACCCTCAAGCCGTTATAACGCCAACGAGTGCCAACGATGATGGTTT	60
1	<u>M T A E T L K P F I T P T S A N D D G F</u>	20
61	CGGGCCAAAGCGACCAGCACGGCGACCGCCCAGCGACGCACCCGCCAGCTGATCCCCCTG	120
21	<u>P A K A T S T A T A Q R R T R Q L I P L</u>	40
121	GTTTGCGGTTCATCGGTCTGGGCTGGTCGTTGCCATTCTCGCACTAACGATCTGGCAG	180
41	<u>V L G F I G L G L V V A I L A L T I W Q</u>	60
181	ACAACCGCGTGTATCGCATCTGGACAAGGAGCTGAAGAGCCTGAAGCGAGTCGTCGATAAT	240
61	T T R V S H L D K E L K S L K R V V D N	80
241	CTCCAGCAGCGTTGGGCATAAAACTATCTGGACGAGTCGACGAGTTCCAAAAGGAGTAC	300
81	L Q Q R L G I N Y L D E F D E F Q K E Y	100
301	GAGAATGCCCTCATCGACTATCCAAAAAGGTGGATGGCCTCACGGATGAGGAGGACGAC	360
101	E N A L I D Y P K K V D G L T D E E D D	120
361	GACGATGGCGATGGTCTGGATTCCATTGGCGACGACGAGGACGACGACGTTAGCTATAGC	420
121	D D G D G L D S I A D D E D D D V S Y S	140
421	TCTGTGGATGATGTTGGCGCAGACTACGAGGACTACACCGATATGTTAAATAACTCAAC	480
141	S V D D V G A D Y E D Y T D M L N K L N	160
481	AATGCACATACCGGCACCACGCCACATCTGAGACCACTGCTGAGGGCGAGGGCGAGACG	540
161	N A H T G T T P T S E T T A E G E G E T	180
541	GACAGTGCATCCTCAGCCTCAAATGATGACAATGTGTCGATGACTTACAGCTACAAT	600
181	D S A S S A S N D D N V F D D F T S Y N	200
601	GCCCACAAAAAGAACGGAGAGAAAATCTCGCTCGATTGCCGATGTACGCAATGAGGAG	660
201	A H K K K Q E R K S R S I A D V R N E E	220
661	CAGAATATTCAAGGAAATCACACAGAGCTTCAGGAAAAGTCATCCAATGAGGCAACTTCC	720
221	Q N I Q G N H T E L Q E K S S N E A T S	240
721	AAAGAGAGAATGCATTCCGCCATGCCACCTCCTAGTCCGCAAAGGTGAATCTCTTCTT	780
241	K E R M H S R H R H L L V R K G E S L L	260
781	TCAGCCAGATCCGAGGACTCGAGGCCAGCAGCCCATTCCACTTGAGCAGCAGGCGCGT	840
261	S A R S E D S R P A A H F H L S S R R R	280
841	CACCAAGGAAGTATGGGCTACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAC	900
281	H Q G S M G Y H G D M Y I G N D N E R N	300

Figure 2B

901	TCTTATCAGGGACACTTC	CAAACGCGCGATGGCGTCTTGACGGTGACCAATA	CAGGCCTA	960	
301	S Y Q G H F Q T R D G V	L T V T N T G I		320	
961	TATTACGTATA	CGCCCAGATATGCTACAACA	ACTCGCACGACCAGAACGGATT	TATCGTC	1020
321	Y Y V Y A Q I C Y	N N S H D Q N G F I V		340	
1021	TTTCAAGGAGACACTCC	ATTCCCTGCAGTGCTTGAA	ACACGGTGCCAACCAACATGCCACAT		1080
341	F Q G D T P F L Q C L N T V P T N M P H			360	
1081	AAGGTGCACACCTGCCACACGAGTGGTCTGATCCAC	CTGGAACGAAACGAGAGGATCCAT			1140
361	K V H T C H T S G L I H L E R N E R I H				380
1141	CTGAAGGACATT	CACAACGATCGCAATGCAGTTCTGCGGGAGGGAA	ACAACCGAAGCTAC		1200
381	L K D I H N D R N A V L R E G N N R S Y				400
1201	TTTGGCATCTTCAAGGTGTAA	1221			
401	F G I F K V	406			

Figur 3A

1	GGCACGAGGCGAACGGACGTTAAAGT GAGAAAAGAAACGGTAAATCAGAGATCCCAAG	60
61	CAAGCGCGTGCATGATAGCGAAGAAAAAGCTATCCGTTCACTTAACCTTAC	120
121	CAAGATTGAATTCGCCATCGGGCAAATTACTAAAAATACATAAGTGCAACTCGTCCACT	180
181	GTGTGTTGTGTTTTTTTTGGTTTCGCTGTGCCTTATCGCAAACAAGAAC	240
241	TGATAAAACTAGAAAATATCTTGAGAACTTGTTTCGCGCTTCTTGCTAATTGCC	300
301	GATCGCGGAAGAGAAAAACAAGCAGTAGACAAAACAAGTGTGTAATACAATCTGAAAAG	360
361	GGCACCATCAGCAGCCCCGAGGGGTTATCTATATAGATGTCGCAGCTTATCATCTCATGC	420
421	TGTCTGTGAGGTTGTTCTGTGTGCTCGTAGTATCTTAAATACATAGAGTGTGTTCATA	480
481	TAAAGTGCACAAAGCTCGATTGGAAACAGCTGTCGAGTGCCTTGAGTGGTGGCAAG	540
541	ATCGTCATCATCATCATCGTCGTCATTATCACAGAACAGCATCAGCATCTGGAGGCC	600
601	CGGTTGCTCTAAGATCCCCAGTGTTCATCAATTATGACTGCCGAGACCCTCAAGCCGTTT	660
1	<u>M T A E T L K P F</u>	9
661	ATAACGCCAACGAGTGCCAACGATGATGGTTCCGGCAAAGCGACCAGCACGGCGACC	720
10	<u>I T P T S A N D D G F P A K A T S T A T</u>	29
721	GCCCAGCGACGCACCCGCCAGCTGATCCCCCTGGTTTGGGGTCATCGGTCTGGGCTG	780
30	<u>A Q R R T R Q L I P L V L G F I G L G L</u>	49
781	GTCGTTGCCATTCTCGCACTAACGATCTGGCAGACAAACGCGTGTATCGCATCTGGACAAG	840
50	<u>V V A I L A L T I W Q T T R V S H L D K</u>	69
841	GAGCTGAAGAGCCTGAAGCGAGTCGTCGATAATCTCCAGCAGCGTTGGGCATAAACTAT	900
70	<u>E L K S L K R V V D N L Q Q R L G I N Y</u>	89
901	CTGGACGAGTTCGACGAGTTCCAAAAGGAGTACGAGAATGCCCTCATCGACTATCCAAAA	960
90	<u>L D E F D E F Q K E Y E N A L I D Y P K</u>	109
961	AAGGTGGATGGCCTCACGGATGAGGAGGACGACGATGGCGATGGTCTGGATTCCATT	1020
110	<u>K V D G L T D E E D D D G D G L D S I</u>	129

Figur 3B

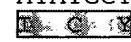
1021	GC GG ACG ACG AGG ACG ACG AC GCT TAG C T A G C T G T G G A T G T G T G G C G C A G A C T A C	1080
130	A D D E D D D V S Y S S V D D V G A D Y	149
1081	GAG GACTACACCGATATGTTAAATAAACTCAACAAATGCACATACCGGCACCACGCCACA	1140
150	E D Y T D M L N K L N N A H T G T T P T	169
1141	TCTGAGACC ACTGCTGAGGGCGAGGGCGAGACGGACAGTGCATCCTCAGCCTCAAATGAT	1200
170	S E T T A E G E G E T D S A S S A S N D	189
1201	GACAATGTGTTCGATGACTTTACAGCTACAATGCCAACAAAAAGAAGCAGGAGAGAAAA	1260
190	D N V F D D F T S Y N A H K K K Q E R K	209
1261	TCTCGCTCGATTGCCGATGTACGCAATGAGGAGCAGAATATTCAAGGAAATCACACAGAG	1320
210	S R S I A D V R N E E Q N I Q G N H T E	229
1321	CTTCAGGAAAAGTCATCCAATGAGGCAACTTCCAAAGAGAGGCCCTGCACCACTTCACAC	1380
230	L Q E K S S N E A T S K E S P A P L H H	249
1381	CGTCGCAGAATGCATTCCGCCATGCCACCTCTAGTCCGCAAAGCCAGATCCGAGGAC	1440
250	R R R M H S R H R H L L V R K A R S E D	269
1441	TCGAGGCCAGCAGCCCATTCCACTTGAGCAGCAGGCCGCTCACCAAGGAAGTATGGC	1500
270	S R P A A H F H L S S R R R H Q G S M G	289
1501	TACCATGGAGATATGTACATAGGAAATGATAACGAGAGAAACTCTTATCAGGGACACTTT	1560
290	Y H G D M Y I G N D N E R N S Y Q G H F	309
1561	CAAACGCGCGATGGCGTCTTGACGGTGACCAATACAGGCCTATATTACGTATACGCCAG	1620
310	Q T R D G V 	329
1621	ATATGCTACAACAACCTCGCACGACCAGAACGGATTATCGTCTTCAGGGACACTCCA	1680
330	 N N S H D Q N G F I V F Q G D T P	349
1681	TTCCTGCAGTGCTTGAACACGGTCCCCACCAACATGCCACATAAGGTGCACACCTGCCAC	1740
350	F L Q C L N T V P T N M P H K V H T C H	369
1741	ACGAGTGGTCTGATCCACCTGGAACGAAACGAGAGAGGATCCATCTGAAGGACATTACAAC	1800
370	T S G L I H L E R N E R I H L K D I H N	389
1801	GATCGCAATGCAGTTCTGCGGGAGGGAAACAACCGAACGAGCTACTTGGCATCTTCAAGGTG	1860
390	D R N A V L R E G N N R S Y F G I F K V	409
1861	TAAATTGGAGAGATTATCCCCGGTCAGAAGATGGAATACCAGTTAAGCTTTGTCCCCG	1920

Figure 3C

1921	CGACTGCTCGTGAATGCGATTCATGCCAGCGTGAATCCATTAGTCGTAGTACCTAGTC	1980
1981	TTAGTCACTCCAAACCTAATCTCAATCGGAATCGTGCATACTGCATTAGTCAGAAGACGG	2040
2041	AGGAAAATCATATTTATTTGTATATACTCGTTCGACTCTAAAAAGTGAATAAAATATA	2100
2101	TGTAGCTATTAAAAAAAAAAAAAAAAAAAAAAAAAAACTCGAG	2148

Figur 4

DmTNF	1	50
DmTNFv1	(1)	MTAETLKP FITPTS <u>SANDGFP</u> AKATSTATAQRRTQLIPLVLGFIGLGLV
DmTNFv2	(1)	MTAETLKP FITPTS <u>SANDGFP</u> AKATSTATAQRRTQLIPLVLGFIGLGLV
DmTNF	51	100
DmTNFv1	(51)	VAILALTIWQTTRVSHLDKELKSLKRVVVDNLQQRLGINYLDEFDEFQKEY
DmTNFv2	(51)	VAILALTIWQTTRVSHLDKELKSLKRVVVDNLQQRLGINYLDEFDEFQKEY
DmTNF	101	150
DmTNFv1	(101)	ENALIDYPKKV DGLTDEEDDDDG GLD SIA D DEDDDDV SYSSVDDVGADYE
DmTNFv2	(101)	ENALIDYPKKV DGLTDEEDDDDG GLD SIA D DEDDDDV SYSSVDDVGADYE
DmTNF	151	200
DmTNFv1	(151)	DYT DMLNKLNNAAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTS SD
DmTNFv2	(151)	DYT DMLNKLNNAAHTGTTPTSETTAEGEGETDSASSASNDDNVFDDFTS YN
DmTNF	201	250
DmTNFv1	(201)	A H KKKQERKSRSIADVRN EEQNIQGNHTELQE KSSNEA SKESPAALH R
DmTNFv2	(201)	A H KKKQERKSRSIADVRN EEQNIQGNHTELQE KSSNEA SKESPA LH HR
DmTNF	251	300
DmTNFv1	(251)	RRMHSR RHLVVRK -----ARSED SRPAAHFH LS RRRH QESMGYHGDM
DmTNFv2	(243)	RRMHSR RHLVVRK GESLLSARSED SRPAAHFH LS RRRH QESMGYHGDM
DmTNFv2	(251)	RRMHSR RHLVVRK -----ARSED SRPAAHFH LS RRRH QESMGYHGDM
DmTNF	301	350
DmTNFv1	(295)	Y IENDRERCSYQGHFQTRDGVLTVTN AGLYYYVAQIC WCM N NSHDQNGFIVF
DmTNFv2	(292)	Y IENDRERNSYQGHFQTRDGVLTVTN AGLYYYVAQIC WCM N NSHDQNGFIVF
DmTNFv2	(295)	Y IENDRERNSYQGHFQTRDGVLTVTN AGLYYYVAQIC WCM N NSHDQNGFIVF
DmTNF	351	400
DmTNFv1	(345)	QGDTPFLQCLNTVPTNMPHKVHTC TSGLIHLERNERIHLKD IHNDRNAV
DmTNFv2	(342)	QGDTPFLQCLNTVPTNMPHKVHTC TSGLIHLERNERIHLKD IHNDRNAV
DmTNFv2	(345)	QGDTPFLQCLNTVPTNMPHKVHTC TSGLIHLERNERIHLKD IHNDRNAV
DmTNF	401	415
DmTNFv1	(395)	LREGNNR SYFGIFKV
DmTNFv2	(392)	LREGNNR SYFGIFKV
DmTNFv2	(395)	LREGNNR SYFGIFKV

Figure 5

AC005974 : DS05033 (P1 D347), DS01913 (P1 D350). Finished; 158983 bases.
Length = 158,983

Minus Strand HSPs:

Score = 77 (27.1 bits), Expect = 5.5, P = 1.0
Identities = 20/58 (34%), Positives = 31/58 (53%), Frame = -1

Query: 203 NGKLIIVNQDG~~F~~YYLYANICFRH-HETSGDLA---TEYLQLMVYV-TKTSIKIPSSHT 254
+G L V G YY+YA IC+ + H+ +G + T +LQ + V T K+ + HT
Sbjct: 129394 DGVLTVTNTGLYYVYAQICYNNSHDQNGFIVFQGDTPFLQCLNTVPTNMMPHKVHTCHT
129221

Score = 45 (15.8 bits), Expect = 79., Sum P(2) = 1.0
Identities = 9/17 (52%), Positives = 10/17 (58%), Frame = -1

Query: 28 GPLHAPP--PPAPHQPP 42
GP PP PP+P PP
Sbjct: 132361 GPSLPPPFP~~PP~~SPRTPP 132311

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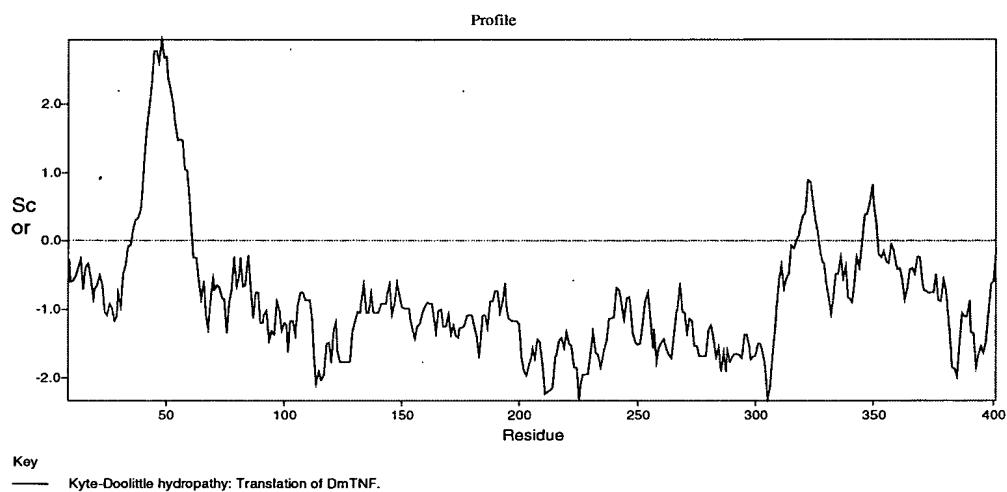
Figure 6A

<p>DmTNF DmTNFv1 DmTNFv2 Osteoprotegerin hCD27L hCD30L hTRAIL hEctodysplasmin_A mEctodysplasmin_A</p> <p>DmTNF DmTNFv1 DmTNFv2 Osteoprotegerin hCD27L hCD30L hTRAIL hEctodysplasmin_A mEctodysplasmin_A</p> <p>DmTNF DmTNFv1 DmTNFv2 Osteoprotegerin hCD27L hCD30L hTRAIL hEctodysplasmin_A mEctodysplasmin_A</p> <p>DmTNF DmTNFv1 DmTNFv2 Osteoprotegerin hCD27L hCD30L hTRAIL hEctodysplasmin_A mEctodysplasmin_A</p> <p>DmTNF DmTNFv1 DmTNFv2 Osteoprotegerin hCD27L hCD30L hTRAIL hEctodysplasmin_A mEctodysplasmin_A</p> <p>DmTNF DmTNFv1 DmTNFv2 Osteoprotegerin hCD27L hCD30L hTRAIL hEctodysplasmin_A mEctodysplasmin_A</p> <p>DmTNF DmTNFv1 DmTNFv2 Osteoprotegerin hCD27L hCD30L hTRAIL hEctodysplasmin_A mEctodysplasmin_A</p>	<p>1</p> <p>(1) --MTAETLKPFITPTSANDDCFPAKATSTATAQR----- (1) --MTAETLKPFITPTSANDDCFPAKATSTATAQR----- (1) --MTAETLKPFITPTSANDDCFPAKATSTATAQR----- (1) -----MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAP (1) ----- (1) ----- (1) -----MAMMEVQGGP----- (1) MGYPVERRELIPAAAPRERGSQGCCGGAPARA----- (1) MGYPVERRELIPAAAPRERGSQGCCCRGAAPARA-----</p> <p>51</p> <p>(33) -----RTROLIPLVLGFIGLCIVMAILALTIWQTTRVSHLDKELKSLKRVV (33) -----RTROLIPLVLGFIGLCIVMAILALTIWQTTRVSHLDKELKSLKRVV (33) -----RTROLIPLVLGFIGLCIVMAILALTIWQTTRVSHLDKELKSLKRVV (39) HQPPAASRSRMFVALLGLGLGQVMCSVALFFYFRAQMDPN-----RISE (1) ----- (1) ----- (1) ----- (11) -----SLGOTCVLIMIFTVLQLSTCMAVTYVFTNEI-----KOMQ (35) -----GEGNSCLLFLGFFGLSDAHLHTLCCYLELRS-----ELRRER (35) -----GEGNSCRLFLGFFGLSDAHLHTLCCYLELRS-----ELRRER</p> <p>101</p> <p>(79) DNLQQRLGINYLDEFDEFQKEYENALIDYPKKVDGLTDEEDDDGDDGLDS (79) DNLQQRLGINYLDEFDEFQKEYENALIDYPKKVDGLTDEEDDDGDDGLDS (79) DNLQQRLGINYLDEFDEFQKEYENALIDYPKKVDGLTDEEDDDGDDGLDS (82) DGTHCIYR-----ILRLHENADFQTTLESQDT----- (1) ----- (1) ----- (1) ----- (47) DKYSKS--G-----IACFLKEDESYWDPNDEES----- (73) GAESRLGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGEAA (73) GTESRLGGPGAPGTSGTLSSPGSLDFVGPITSHLGQPSFQQQPLEPGEDP</p> <p>151</p> <p>(129) HADDEDDEDVSYSISVDDVGADYEDYTDMLNKLNNNAHGTTPTSSETTAEGEG (129) HADDEDDEDVSYSISVDDVGADYEDYTDMLNKLNNNAHGTTPTSSETTAEGEG (129) HADDEDDEDVSYSISVDDVGADYEDYTDMLNKLNNNAHGTTPTSSETTAEGEG (110) -----KLIPDSCRRIKQAFQGAVKOELQHIVGSQHRAE (110) ----- (1) -----MPEEGSGCSVRPRPYGCVLRAALVPL (1) -----MDPGLQQAALNGMAPPGDTAMHPAGSVAS (73) -----MN--SPCQVKWQLRQLVRLMILRTSEETISTVQ (123) HSQDGHQMLINFFFFPDEKPYSEEEESR--VRNKRSKSNEGADGPV (123) UPQDSQDRHQMLINFFFFPDEKAYSEEEESR--VRNKRSKSGEGADGPV</p> <p>201</p> <p>(179) ETD-SASSAISNDNVFDDFTSSDALKKQERKSRSTADVRNEEQNIOGNH (179) ETD-SASSAISNDNVFDDFTSYNAHKKKQERKSRSTADVRNEEQNIOGNH (179) ETD-SASSAISNDNVFDDFTSYNAHKKKQERKSRSTADVRNEEQNIOGNH (144) KAMVDG-----SWLDIAK----- (27) VAG-----LVICLMVCHQR----- (30) HLGTTSRSYFYLTATTALCLVFTVATIMVLVVQRTDSIPN----- (105) EKQQ-----NISPIVR----- (171) KNK-KKGKKAGPPGPNPGPPGPPGPGPQGPPGIPGTPGTPG--TTVMGPP (171) KNK-KKGKKAGPPGPNPGPPGPPGPGPQGPPGIPGTPGTPG--TTVMGPP</p> <p>251</p> <p>(228) TELQEKSSEAAASKESPAALHLRRRMHSRHRHLVMR-----ARSEDLSR (228) TELQEKSSEAAKSKE-----RMHSRHRHLVREGESLLSARSSEDLSR (228) TELQEKSSEAAKSKEPAPLHHRRRMHSRHRHLVMR-----ARSEDLSR (157) -----RSKLEAQP----- (41) -----FAQAOQQOLPLES----- (71) -----SEDNVPLKGGN-----CSED (116) -----ERGP-----RVAAHITCTR----- (218) GPPGPPGPQGPPGLQGP-----SGAADKACTR-----ENQP (218) GPPGPPGPQGPPGLQGP-----SGAADKTCTR-----ENQP</p> <p>300</p>
--	--

Figur 6B

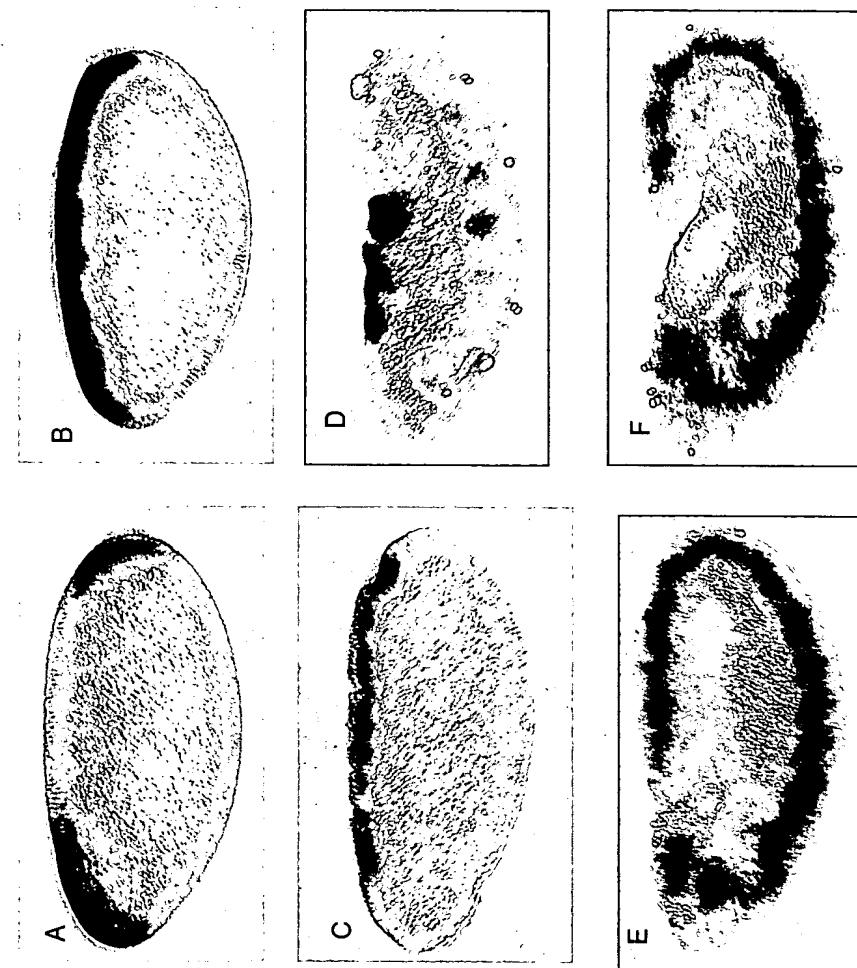
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DmTNF	(272) PAAHFHLSSRRRHQESMGYHCDMYIENDRER-CSYQGHETQRDGVLTVTN
DmTNFv1	(269) PAAHFHLSSRRRHQGSMGYHCDMYIGNDNER-NSYQGHETQRDGVLTVTN
DmTNFv2	(272) PAAHFHLSSRRRHQGSMGYHCDMYIGNDNER-NSYQGHETQRDGVLTVTN
Osteoprotegerin	(165) --FAHTINATDIPSG-ShKVSISSWYHDRG-WKFSNMTFSNGKLIVNQ
hCD27L	(53) --LGWDVIELQLNHTGPQQDPRYWQGGPALGRSEPHGPELDKCOLRTHR
hCD30L	(86) LLCILKRAPFKKSWAYLQVAKHLNKTLSWNKDGIIHGVRYODGNLVHQF
hTRAIL	(131) -GRSN-TLSSPNSKNEALGRKHSNSWESSRSRGHSEPSNHLRNGELVTHE
hEctodysplasmin_A	(249) AVVHLQGGSQAIQVKNDLSCGVENDWSRITM-NEKMFKEHPRSGELEVLV
mEctodysplasmin_A	(249) AVVHLQGGSQAIQVKNDLSCGVENDWSRITM-NEKMFKEHPRSGELEVLV
351	400
DmTNF	(321) AGIYYVYVY-----AQIWWGYNSHDONGEITVEQG-DTPFLQCUNIVPTNM
DmTNFv1	(318) TGEYYVYVY-----AQIWCYNNSHDONGEITVEQG-DTPFLQCENIVPTNM
DmTNFv2	(321) TGEYYVYVY-----AQIWCYNNSHDONGEITVEQG-DTPFLQCENIVPTNM
Osteoprotegerin	(211) DGEYYVYVYANICFRHHETSGDLATEYLQLMVYWTKTGKIEPSSHTLMKGGS
hCD27L	(101) DGTYYVHIQVTLAICSSITASRHHPTILAVGTCSS-PASRSISLRLSF
hCD30L	(136) PGTYPTTICQLQFLVQCPNNSVDLKELLINKHKKGALVTVCESGMQTKH
hTRAIL	(179) KGEYYVYVYSOTYFRFQEEIKENIKNDKOMVQYHYK-YTSPDPILLMKSAR
hEctodysplasmin_A	(298) DGTYYVYVYSQ-----VEMYYINFTDFASMEVWVD-BKPFLQCTRSTETGK
mEctodysplasmin_A	(298) DGTYYVYVYSQ-----VEMYYINFTDFASMEVWVD-BKPFLQCTRSTETGK
401	450
DmTNF	(362) PHK-----VHTCHTSGLIHLERNERIHDKDITHDRNAVEREGNNRSY
DmTNFv1	(359) PHK-----VHTCHTSGLIHLERNERIHDKDITHDRNAVEREGNNRSY
DmTNFv2	(362) PHK-----VHTCHTSGLIHLERNERIHDKDITHDRNAVEREGNNRSY
Osteoprotegerin	(261) TKYWSGNSEFHFMISIVGCGFKURSCEEFISTEVSNPSLIDPDQ---DATV
hCD27L	(148) HQG-----CTIVSORUTPLAREDDTCTNLTGTLPSRNT---DETF
hCD30L	(186) VYQN-----LSQFLLDYLVQVNTTISVNMDTFQYIDTSTFPLENVI
hTRAIL	(228) NSCWSKDAEYGLYSIMOGGIFELKENDRIFVSVTNEHIDMDH---EASF
hEctodysplasmin_A	(341) TN-----YNTCYTAGVCLLKA R OKIAV K MV H ADISINMS--KHTTF
mEctodysplasmin_A	(341) TN-----YNTCYTAGVCLLKA R OKIAV K MV H ADISINMS--KHTTF
451	462
DmTNF	(404) FGIFKV-----
DmTNFv1	(401) FGIFKV-----
DmTNFv2	(404) FGIFKV-----
Osteoprotegerin	(308) FGAFKVRDID--
hCD27L	(186) FGVWWRP-----
hCD30L	(226) SIFLYNSND---
hTRAIL	(275) FGAFLVG-----
hEctodysplasmin_A	(380) FGATRUEGEAPAS
mEctodysplasmin_A	(380) FGATRUEGEAPAS

Figure 7



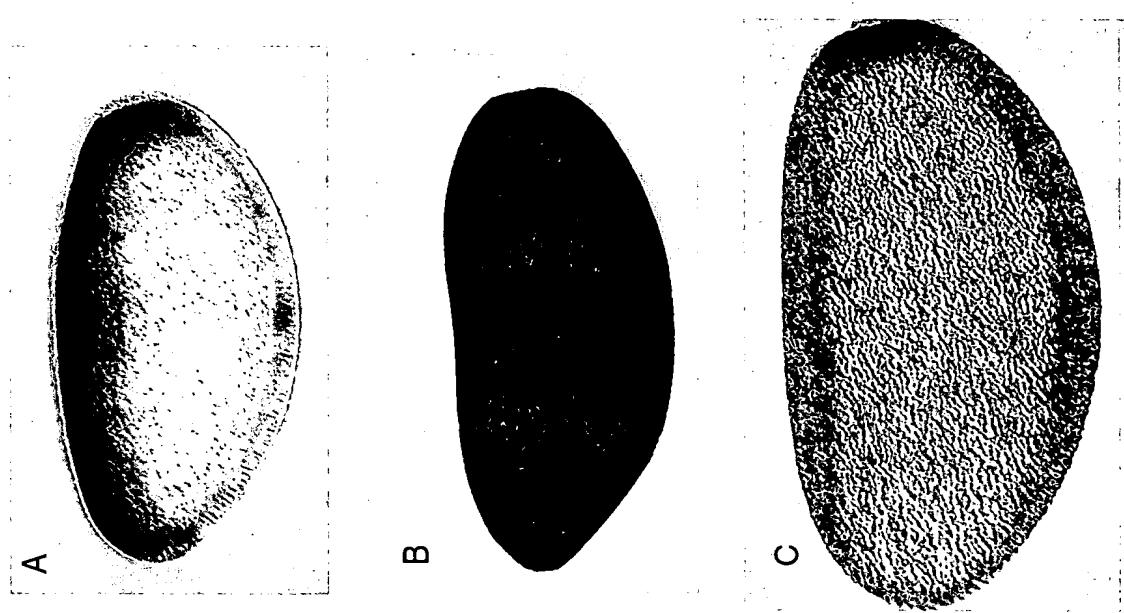
www.ncbi.nlm.nih.gov/blast/blast.cgi
http://blast.ncbi.nlm.nih.gov/Blast.cgi

Figure 8



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DOI: 10.1002/jinpa.10003

Figure 9



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Figure 10

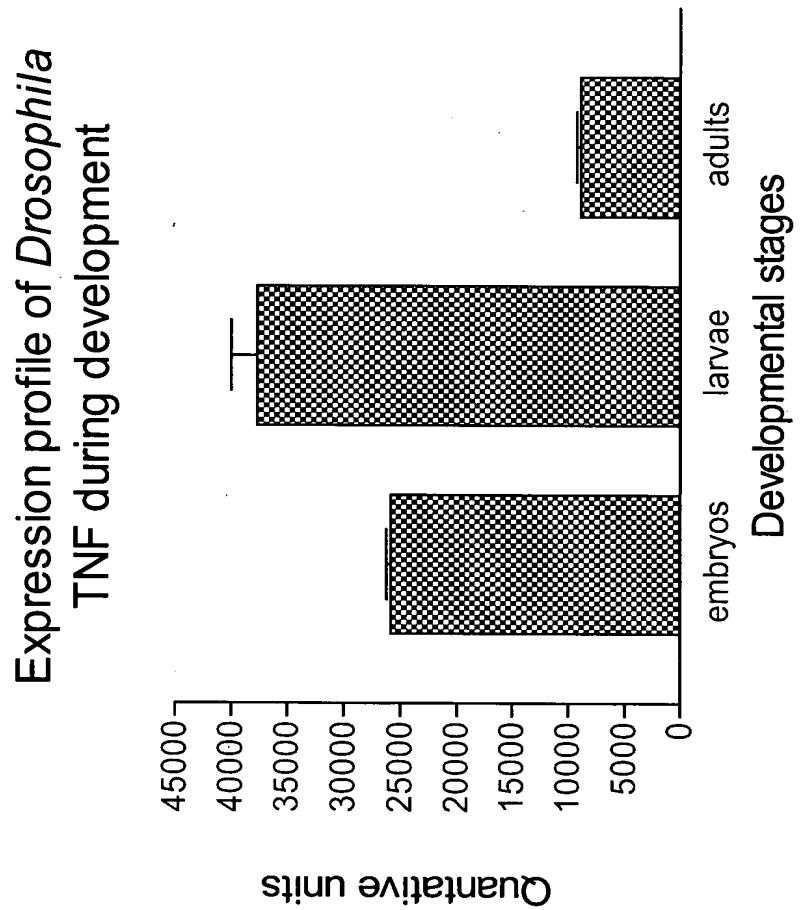


Figure 11

DmTNF

Protein	Genbank ID	Identities	Similarities
human osteoprotegerin protein	gil12643360	21.4%	35.7%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	24.6%	34.4%
human ectodysplasmin_A protein	gilQ92838	21.2%	27.9%
mouse ectodysplasmin_A protein	gilNP_034229	20.4%	28.5%

DmTNFv1

Protein	Genbank ID	Identities	Similarities
human osteoprotegerin protein	gil12643360	23.8%	30.5%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	23.3%	32.7%
human ectodysplasmin_A protein	gilQ92838	21.8%	28.6%
mouse ectodysplasmin_A protein	gilNP_034229	21%	28.6%

DmTNFv2

Protein	Genbank ID	Identities	Similarities
human osteoprotegerin protein	gil12643360	21.4%	35.7%
human hCD27 ligand protein	gil P32970	12.5%	37.5%
human CD30 ligand protein	gil P32971	20%	26.7%
human TRAIL protein	gil P50591	24.1%	33.9%
human ectodysplasmin_A protein	gilQ92838	22.4%	29.1%
mouse ectodysplasmin_A protein	gilNP_034229	21.6%	29.2%

Figure 12

